MYCOTAXON

ISSN (print) 0093-4666 (online) 2154-8889 Mycotaxon, Ltd. ©2019

October–December 2019—Volume 134, pp. 649–662

https://doi.org/10.5248/134.649

Rhomboidia wuliangshanensis gen. & sp. nov. from southwestern China

Tai-Min Xu[1,2], Xiang-Fu Liu[3], Yu-Hui Chen[2], Chang-Lin Zhao[1,3*]

[1] *Yunnan Provincial Innovation Team on Kapok Fiber Industrial Plantation;*
[2] *College of Life Sciences;* [3] *College of Biodiversity Conservation:*
Southwest Forestry University, Kunming 650224, P.R. China

[*] Correspondence to: *fungichanglinz@163.com*

Abstract—A new, white-rot, poroid, wood-inhabiting fungal genus, *Rhomboidia*, typified by *R. wuliangshanensis*, is proposed based on morphological and molecular evidence. Collected from subtropical Yunnan Province in southwest China, *Rhomboidia* is characterized by annual, stipitate basidiomes with rhomboid pileus, a monomitic hyphal system with thick-walled generative hyphae bearing clamp connections, and broadly ellipsoid basidiospores with thin, hyaline, smooth walls. Phylogenetic analyses of ITS and LSU nuclear RNA gene regions showed that *Rhomboidia* is in *Steccherinaceae* and formed as distinct, monophyletic lineage within a subclade that includes *Nigroporus*, *Trullella*, and *Flabellophora*.

Key words—*Polyporales,* residual polyporoid clade, taxonomy, wood-rotting fungi

Introduction

Polyporales Gäum. is one of the most intensively studied groups of fungi with many species of interest to fungal ecologists and applied scientists (Justo & al. 2017). Species of wood-inhabiting fungi in *Polyporales* are important as saprobes and pathogens in forest ecosystems and in their application in biomedical engineering and biodegradation systems (Dai & al. 2009, Levin & al. 2016). With roughly 1800 described species, *Polyporales* comprise about 1.5% of all known species of Fungi (Kirk & al. 2008). Currently, there are 46 genomes of polyporalean taxa available from the Joint Genome Institute MycoCosm portal (Grigoriev & al. 2013).

Table 1. Species and sequences used in the phylogenetic analyses

Species	Sample	GenBank accession no.		References
		ITS	LSU	
Abortiporus biennis	TFRI 274	EU232187	EU232235	Larsson 2007
Antrodiella americana	Gothenburg 3161	JN710509	JN710509	Miettinen & al. 2012
A. semisupina	FCUG 960	EU232182	EU232266	Binder & al. 2005
Antrodiella sp.	X 418	JN710523	JN710523	Miettinen & al. 2012
Climacocystis borealis	KH 13318	JQ031126	JQ031126	Binder & al. 2013
Diplomitoporus flavescens	X 84	FN907908	—	Miettinen & al. 2012
Elaphroporia ailaoshanensis	CLZhao 595	MG231568	MG231568	Wu & al. 2018
	CLZhao 596	MG231572	MG231572	Wu & al. 2018
Flabellophora sp.	X340	JN710534	JN710534	Miettinen & al. 2012
Flaviporus brownii	X 1216	JN710537	JN710537	Miettinen & al. 2012
F. liebmannii	X 251	JN710541	JN710541	Miettinen & al. 2012
	X 249	JN710539	JN710539	Miettinen & al. 2012
	X 666	JN710540	JN710540	Miettinen & al. 2012
Frantisekia mentschulensis	BRNM 710170	FJ496728	—	Tomšovský & al. 2010
	1377	JN710544	JN710544	Miettinen & al. 2012
Hypochnicium bombycinum	MA 15305	FN552537	—	Binder & al. 2013
H. lyndoniae	NL 041031	JX124704	JX124704	Binder & al. 2005
Irpex lacteus	CBS 431.48	MH856423	MH867969	Vu & al. 2019
	DO 421/951208	JX109852	JX109852	Binder & al. 2013
Ischnoderma benzoinum	KHL 12099	JX109841	JX109841	Binder & al. 2013
I. resinosum	FD-328	KP135303	KP135225	Floudas & Hibbett 2015
Junghuhnia crustacea	X 1127	JN710554	JN710554	Miettinen & al. 2012
	X 262	JN710553	JN710553	Miettinen & al. 2012
J. micropora	Spirin 2652	JN710559	JN710559	Miettinen & al. 2012
Loweomyces fractipes	X 1149	JN710570	JN710570	Miettinen et al. 2012
	X 1253	JN710569	JN710569	Miettinen & al. 2012
	X 1250	JN710568	JN710568	Miettinen & al. 2012
Mycorrhaphium adustum	8024	JN710573	JN710573	Miettinen & al. 2012
	Dai 10173	KC485537	KC485554	—

Nigroporus vinosus	X 839	N710576	N710576	Miettinen & al. (012
	8182	JN710728	JN710728	Miettinen & al. 2012
	BHS2008-100	JX109857	JX109857	Binder & al. 2013
Panus conchatus	X 1234	JN710579	JN710579	Miettinen & al. 2012
P. strigellus	INPA 243940	JQ955725	JQ955732	Binder & al. 2013
Physisporinus sanguinolentus	BRNM 699576	FJ496671	FJ496725	Tomšovský & al. 2010
P. vitreus	3163	JN710580	JN710580	Miettinen & al. 2012
	KHL11959	JQ031129	JQ031129	Sjökvist & al. 2012
	CBS 486.72	MH860538	MH872244	Vu & al. 2019
Podoscypha venustula	CBS 65684	JN649367	JN649367	Binder & al. 2013
Pseudolagarobasidium acaciicola	CBS 115543	DQ517883	—	Miettinen & Rajchenberg 2012
	CBS 115544	DQ517882	—	Miettinen & Rajchenberg 2012
P. belizense	CFMR DLC 04-31	JQ070173	—	Miettinen & Rajchenberg 2012
Rhomboidia wuliangshanensis	**CLZhao 4406 [T]**	MK860715	MK860710	Present study
	CLZhao 4411	MK860716	MK860711	Present study
Skeletocutis novae-zelandiae	Ryvarden 38641	JN710582	JN710582	Miettinen & al. 2012
Spongipellis spumeus	PRM 891931	HQ728287	HQ729021	Tomšovský & al. 2010
	BRNM 712630	HQ728288	HQ728288	Tomšovský & al. 2010
	BRNM 734877	HQ728283	HQ728283	Tomšovský & al. 2010
Steccherinum fimbriatum	KHL 11905	EU118668	EU118668	Tomšovský & al. 2010
S. ochraceum	Ryberg s.n.	EU118669	EU118670	Larsson 2007
	KHL 11902	JQ031130	JQ031130	Sjökvist & al. 2012
Trullella dentipora	X 200	JN710512	JN710512	Miettinen & al. 2012
T. duracina	X 290	JN710513	JN710513	Miettinen & al. 2012
T. polyporoides	X 510	JN710602	JN710602	Miettinen & al. 2012
Xanthoporus syringae	X 339	JN710606	JN710606	Miettinen & al. 2012
	Cui 2177	DQ789395	—	Miettinen & al. 2012
	Gothenburg 1488	JN710607	JN710607	Miettinen & al. 2012

Systematics of the *Polyporales* has benefitted from numerous molecular phylogenetic studies (e.g., Binder & al. 2005, 2013; Larsson 2007; Miettinen & al. 2012; Dai & al. 2015; Choi & Kim 2017). *Steccherinaceae* Parmasto, one of 18 families recognized in *Polyporales* (Justo & al. 2017), has been included in several molecular studies (e.g., Binder & al. 2005, 2013; Miettinen & al. 2012; Miettinen & Ryvarden 2016; Justo & al. 2017; Westphalen & al. 2018). Miettinen & al. (2012) published a multigene, molecular phylogenetic study of *Steccherinum* and allied taxa that clearly delineated *Steccherinaceae*. They uncovered surprising morphological diversity and plasticity in this family, requiring revision of generic concepts and 15 new genera to accommodate existing and new species. Subsequently, Miettinen & Ryvarden (2016) introduced five new genera, revised one genus, and described two new species that had been identified earlier by Miettinen & al. (2012). Justo & al. (2017), who revised family-level classification in *Polyporales,* confirmed *Steccherinaceae* as a distinct lineage in *Polyporales* that grouped with *Cerrenaceae* Miettinen & al. and *Panaceae* Miettinen & al. In a morphological and molecular study of Neotropical taxa of *Junghuhnia* and *Steccherinum*, Westphalen & al. (2018) uncovered a new genus and several new species and reclassified four taxa.

Cosmopolitan in distribution, *Steccherinaceae* has a rich diversity because it is found in boreal, temperate, subtropical, and tropical ecosystems (Núñez & Ryvarden 2001, Dai 2012, Ryvarden & Melo 2014, Dai & al. 2015, Zhou & al. 2016). Many new species in *Polyporales* have been described from southern, subtropical China (e.g., Li & Cui 2010, Zhao & Wu 2017, Zhao & Ma 2019). Recently, we collected an undescribed taxon from Yunnan Province that could not be assigned to any described genus. We present morphological and molecular phylogenetic evidence that support the recognition of a new monotypic genus in *Steccherinaceae—Rhomboidia*, typified by *R. wuliangshanensis*.

Materials & methods

The specimens studied are deposited at the herbarium of Southwest Forestry University, Kunming, China (SWFC). Macromorphological descriptions are based on field notes. Special colour terms follow Petersen (1996). Micromorphological data were obtained from the dried specimens and observed under a light microscope following Dai (2010). The following abbreviations are used: KOH = 5% potassium hydroxide; CB = cotton blue; CB– = acyanophilous; IKI = Melzer's reagent; IKI– = non-amyloid and non-dextrinoid; L = mean spore length (arithmetic average of all spores); W = mean spore width (arithmetic average of all spores); Q = variation in

the L/W ratios between the specimens studied; (n = a/b) = number of spores (a) from number of specimens (b).

HiPure Fungal DNA Mini Kit II was used to obtain genomic DNA from dried specimens, according to the manufacturer's instructions with some modifications. A small piece (about 30 mg) of dried fungal material was ground to powder with liquid nitrogen. The powder was transferred to a 1.5 ml centrifuge tube, suspended in 0.4 ml of lysis buffer, and incubated in a 65 °C water bath for 60 min. After that, 0.4 ml phenol-chloroform (24:1) was added to each tube and the suspension was shaken vigorously. After centrifugation at 13,000 rpm for 5 min, 0.3 ml supernatant was transferred to a new tube and mixed with 0.45 ml binding buffer. The mixture was then transferred to an adsorbing column (AC) for centrifugation at 13,000 rpm for 0.5 min. Then, 0.5 ml inhibitor removal fluid was added in AC for a centrifugation at 12,000 rpm for 0.5 min. After washing twice with 0.5 ml washing buffer, the AC was transferred to a clean centrifuge tube, and 100 ml elution buffer was added to the middle of adsorbed film to elute the genomic DNA. The internal transcribed spacer region (ITS) was amplified with primer pairs ITS5 and ITS4 (White & al. 1990). The nuclear large subunit region (LSU) was amplified with primer pairs LR0R and LR7 (https://sites.duke.edu/vilgalyslab/rdna_primers_for_fungi/). The PCR procedure for ITS was: initial denaturation at 95 °C for 3 min, followed by 35 cycles of 94 °C for 40 s, 58 °C for 45 s, and 72 °C for 1 min; and a final extension of 72 °C for 10 min. The PCR procedure for LSU was: initial denaturation at 94 °C for 1 min, followed by 35 cycles of 94 °C for 30 s, 48 °C 1 min, and 72 °C for 1.5 min; and a final extension of 72 °C for 10 min. The PCR products were purified and directly sequenced at Kunming Tsingke Biological Technology Limited Company. All newly generated sequences were deposited at GenBank (Table 1).

Sequencher 4.6 was used to edit the DNA sequence. Sequences were aligned in MAFFT 6 (Katoh & Toh 2008, http://mafft.cbrc.jp/alignment/server/) using the "G-INS-I" strategy and manually adjusted in BioEdit (Hall 1999). The sequence alignment was deposited in TreeBase (submission ID 24216). *Xanthoporus syringae* (Parmasto) Audet obtained from GenBank was used as an outgroup to root trees following Miettinen & al. (2012) in the ITS+LSU analyses (Fig. 1).

The ITS+LSU sequences were analyzed phylogenetically using maximum parsimony, maximum likelihood, and Bayesian inference methods. Maximum parsimony (MP) analyses followed Zhao & Wu (2017), and tree construction was performed in PAUP* version 4.0b10 (Swofford 2002). All characters were equally weighted and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1000 random sequence additions. Max-trees was set to 5000, branches of zero length were collapsed and all parsimonious trees were saved. Clade robustness was assessed using bootstrap (BP) analysis with 1000 replicates (Felsenstein 1985). Tree statistics tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI) were calculated for each Maximum Parsimonious Tree generated. Sequences were analyzed using Maximum Likelihood (ML) with

RAxML-HPC2 through the Cipres Science Gateway (www.phylo.org; Miller & al. 2009). Branch support (BS) for ML analysis was determined by 1000 bootstrap replicates.

MrModeltest 2.3 (Posada & Crandall 1998; Nylander 2004) was used to determine the best-fit evolution model for data set for Bayesian inference (BI). Bayesian inference was calculated with MrBayes_3.1.2 using a general time reversible (GTR+G) model of DNA substitution and a gamma distribution rate variation across sites (Ronquist & Huelsenbeck 2003). Four Markov chains were run for 2 runs from random starting trees for 4 million generations (ITS+LSU) in Fig. 1 and trees were sampled every 100 generations. The first 25% of the generations were discarded as burn-in. A majority rule consensus tree of all remaining trees was calculated. Branches that received bootstrap support for maximum likelihood (BS) ≥75%, maximum parsimony (BP) ≥75%, and Bayesian posterior probabilities (BPP) ≥0.95 were considered significantly supported.

Molecular phylogenetic results

The ITS+LSU (Fig. 1) dataset comprised sequences from 55 fungal specimens representing 34 taxa, including the outgroup taxon. The dataset had an aligned length of 2296 of which 1395 were constant, 201 parsimony-uninformative, and 700 parsimony-informative. MP analysis yielded two equally parsimonious trees (TL = 3897, CI = 0.376, HI = 0.624, RI = 0.627, RC = 0.236). The best-fit model for ITS+LSU alignment estimated and applied in the BI was GTR+I+G, lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). BI resulted in a similar topology with an average standard deviation of split frequencies equal to 0.006862.

Rhomboidia wuliangshanensis forms a monophyletic lineage with strong support (BS = 100%, BP = 100%, BPP = 1) and is sister to the *Nigroporus–Trullella* clade (Fig. 1).

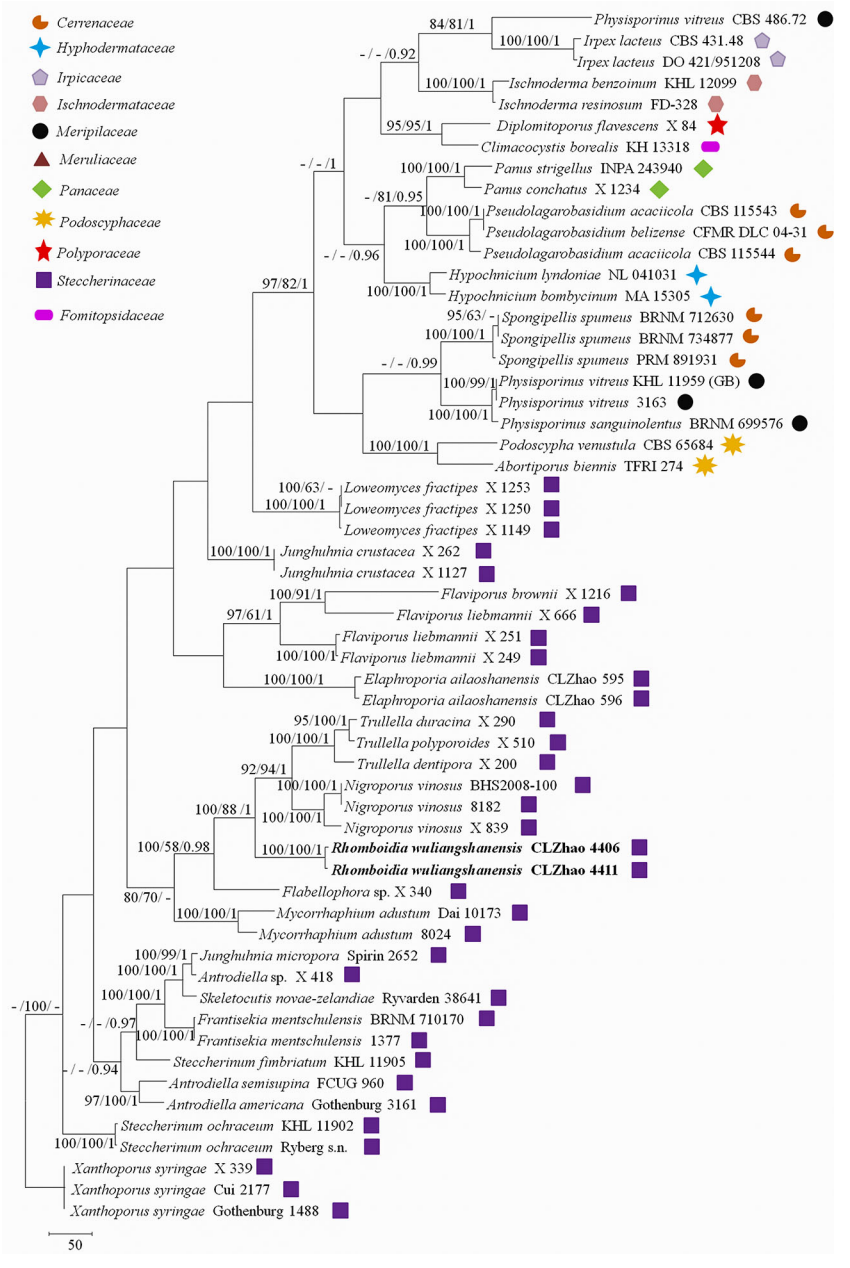
Taxonomy

Rhomboidia C.L. Zhao, **gen. nov.**

MB 833318

Differs from *Nigroporus* and *Trullella* by its stipitate to substipitate basidiomata, its orange-brown to reddish brown surface, and its monomitic hyphal system in both context and trama.

Fig. 1. Maximum parsimony strict consensus tree illustrating the phylogeny of *Rhomboidia wuliangshanensis* and related species in the residual polyporoid clade based on ITS+nLSU sequences. Branches are labeled with maximum likelihood bootstrap >70%, parsimony bootstrap proportions >50% and Bayesian posterior probabilities >0.95.


Cerrenaceae
Hyphodermataceae
Irpicaceae
Ischnodermataceae
Meripilaceae
Meruliaceae
Panaceae
Podoscyphaceae
Polyporaceae
Steccherinaceae
Fomitopsidaceae
Physisporinus vitreus CBS 486.72
Irpex lacteus CBS 431.48
Irpex lacteus DO 421/951208
Ischnoderma benzoinum KHL 12099
Ischnoderma resinosum FD-328
Diplomitoporus flavescens X 84
Climacocystis borealis KH 13318
Panus strigellus INPA 243940
Panus conchatus X 1234
Pseudolagarobasidium acaciicola CBS 115543
Pseudolagarobasidium belizense CFMR DLC 04-31
Pseudolagarobasidium acaciicola CBS 115544
Hypochnicium lyndoniae NL 041031
Hypochnicium bombycinum MA 15305
Spongipellis spumeus BRNM 712630
Spongipellis spumeus BRNM 734877
Spongipellis spumeus PRM 891931
Physisporinus vitreus KHL 11959 (GB)
Physisporinus vitreus 3163
Physisporinus sanguinolentus BRNM 699576
Podoscypha venustula CBS 65684
Abortiporus biennis TFRI 274
Loweomyces fractipes X 1253
Loweomyces fractipes X 1250
Loweomyces fractipes X 1149
Junghuhnia crustacea X 262
Junghuhnia crustacea X 1127
Flaviporus brownii X 1216
Flaviporus liebmannii X 666
Flaviporus liebmannii X 251
Flaviporus liebmannii X 249
Elaphroporia ailaoshanensis CLZhao 595
Elaphroporia ailaoshanensis CLZhao 596
Trullella duracina X 290
Trullella polyporoides X 510
Trullella dentipora X 200
Nigroporus vinosus BHS2008-100
Nigroporus vinosus 8182
Nigroporus vinosus X 839
Rhomboidia wuliangshanensis CLZhao 4406
Rhomboidia wuliangshanensis CLZhao 4411
Flabellophora sp. X 340
Mycorrhaphium adustum Dai 10173
Mycorrhaphium adustum 8024
Junghuhnia micropora Spirin 2652
Antrodiella sp. X 418
Skeletocutis novae-zelandiae Ryvarden 38641
Frantisekia mentschulensis BRNM 710170
Frantisekia mentschulensis 1377
Steccherinum fimbriatum KHL 11905
Antrodiella semisupina FCUG 960
Antrodiella americana Gothenburg 3161
Steccherinum ochraceum KHL 11902
Steccherinum ochraceum Ryberg s.n.
Xanthoporus syringae X 339
Xanthoporus syringae Cui 2177
Xanthoporus syringae Gothenburg 1488
50

Type species: *Rhomboidia wuliangshanensis* C.L. Zhao

Etymology: *Rhomboidia* (Lat.): referring to the rhomboid pileus of the basidiocarp with the poroid hymenophore.

Basidiomata annual, stipitate. Pileus rhomboid, arising from a multiple branched stipe. Pores angular, small, dissepiments thin, entire. Hyphal system monomitic; generative hyphae thick-walled bearing clamp connections, IKI–, CB–; tissues unchanged in KOH. Cystidia absent, fusoid cystidioles numerous; hyphal ends numerous. Basidia barrel-shaped to clavate. Basidiospores broadly ellipsoid, hyaline, thin-walled, smooth, IKI–, CB–.

Type of rot: white rot.

Rhomboidia wuliangshanensis C.L. Zhao, **sp. nov**. Figs 2, 3

MB 833320

Differs from *Nigroporus vinosus* by its stipitate to substipitate basidiomata and monomitic hyphal structure.

Type: China. Yunnan Province: Puer, Jingdong County, Wuliangshan National Nature Reserve, on angiosperm trunk, 6 Oct 2017, CLZhao 4406 (**Holotype**, SWFC 0004406; GenBank MK860715, MK860710).

Etymology: The specific epithet *wuliangshanensis* (Lat.) refers to the type locality, Wuliangshan.

Basidiomata annual, stipitate to substipitate. Pileus rhomboid, arising from a multiple branched stipe, edges curling slightly inward, 3.5 cm from the base to margin, 4 cm wide, up to 3 mm thick; pileus surface radially striate, slightly brown to orange brown when fresh, drying brown to reddish; the margin acute, entire. Pore surface white when fresh, cream to buff upon drying. Pores angular, 7–9 per mm, dissepiments thin, entire. Context corky, white, thin, up to 0.5 mm thick. Tubes concolorous with pore surface, corky, up to 2.5 mm long.

-Type of rot: white rot.

Additional specimen examined: **China**. **Yunnan province**. **Puer:** Jingdong County, Wuliangshan National Nature Reserve, on angiosperm trunk, 6 Oct 2017, CLZhao 4411 (SWFC 004411; GenBank MK860716, MK860711).

Discussion

Rhomboidia is supported as a new genus by phylogenetic analyses and morphological characters. It is embedded in *Steccherinaceae* with strong support. Phylogenetically, *Rhomboidia* is closely related to *Flabellophora* G. Cunn., *Nigroporus* Murrill, and *Trullella* Zmitr. based on ITS+LSU nuclear RNA gene analyses (Fig. 1), which is similar to the previous multigene sequence-based study (Miettinen & al. 2012). The genera closely related to *Rhomboidia*

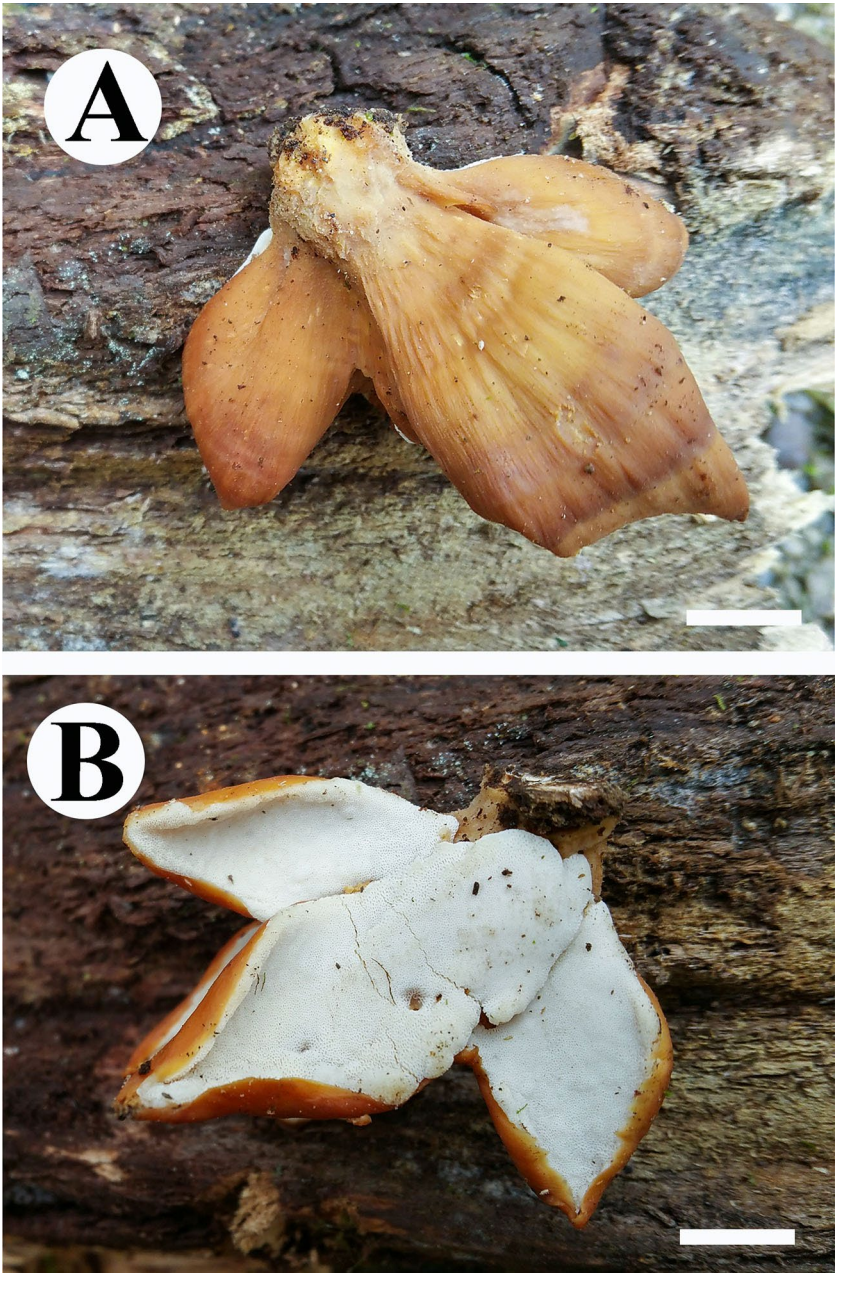


Fig. 2. *Rhomboidia wuliangshanensis* (holotype, SWFC 0004406). Scale bars = 5 mm.

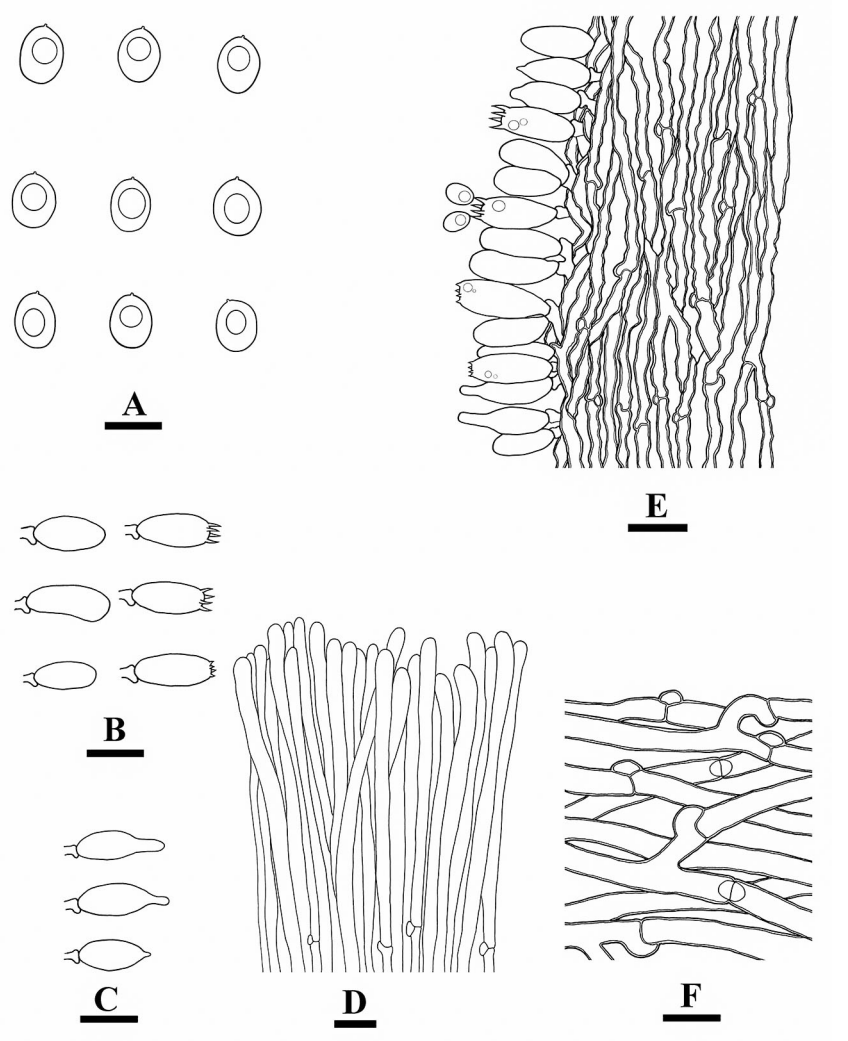


Fig. 3. *Rhomboidia wuliangshanensis* (drawn from the holotype, SWFC 0004406). A. Basidiospores; B. Basidia and basidioles; C. Cystidioles; D. Hyphal ends; E. Hyphae from trama; F. Hyphae from subiculum. Scale bars: a = 5 μm; b–f = 10 μm.

are easily separated morphologically: In *Flabellophora* basidiomata arise from a submerged pseudosclerotium and develop unilateral pilei with a crust and a coriaceous context (Núñez & Ryvarden 2001). *Nigroporus* differs from *Rhomboidia* by developing resupinate to pileate basidiocarps with vinaceous brown to pink or violet pore surface and a dimitic hyphal system (Gilbertson & Ryvarden 1987). In *Trullella* basidiomata are spathulate and light-coloured, with a monomitic hyphal system in the context but dimitic in the trama (Miettinen & al. 2012, Zmitrovich 2018).

Rhomboidia resembles other stipitate genera in *Polyporales* such as *Abortiporus* Murrill, *Jahnoporus* Nuss, and *Polyporus* P. Micheli ex Adans. *Abortiporus*, however, has a duplex structure and thick-walled basidiospores (Núñez & Ryvarden 2001). *Jahnoporus* is characterized by large spindle-shaped basidiospores (Gilbertson & Ryvarden 1987), and *Polyporus* has a dimitic hyphal system (Bernicchia & Gorjón 2010).

Polypores are extensively studied and well-known in North America (Gilbertson & Ryvarden 1987, Zhou & al. 2016) and Eurasia (Núñez & Ryvarden 2001, Bernicchia & Gorjón 2010, Dai 2012, Ryvarden & Melo 2014, Dai & al. 2015), but Chinese polypore diversity is still being explored, especially in subtropical and tropical areas. *Rhomboidia wuliangshanensis* was collected from Yunnan Province, where many new taxa in *Polyporales* and *Hymenochaetales* have been described (e.g., Li & Cui 2010, He & Li 2011, Yu & al. 2013, Yang & He 2014, Zhao & Wu 2017, Zhao & Ma 2019). We anticipate that additional, undescribed polypore taxa will be discovered throughout China after extensive collections are analyzed both morphologically and molecularly.

Acknowledgments

Special thanks are due to Drs. Karen K. Nakasone (Center for Forest Mycology Research, Northern Research Station, U.S. Forest Service, USA) and Lu-Sen Bian (Experiment Center of Forestry in North China, Chinese Academy of Forestry, P.R. China) who reviewed the manuscript. The research is supported by the National Natural Science Foundation of China (Project No. 31700023) and Yunnan Agricultural Foundation Projects (2017FG001-042) and the Yunnan Provincial Innovation Team on Kapok Fiber Industrial Plantation (2018HC014) and the Science Foundation of Education Department in Yunnan (2018JS326).

Literature cited

Bernicchia A, Gorjón SP. 2010. Fungi Europaei 12: *Corticiaceae* l. Edizioni Candusso, Lomazzo. 1007 p.

Binder M, Hibbett DS, Larsson KH, Larsson E, Langer E, Langer G. 2005. The phylogenetic distribution of resupinate forms across the major clades of mushroom-forming fungi (*Homobasidiomycetes*). Systematics and Biodiversity 3: 113–157. https://doi.org/10.1017/S1477200005001623

Binder M, Justo A, Riley R, Salamov A, López-Giráldez F, Sjökvist E, Copeland A, Foster B, Sun H, Larsson E, Larsson KH, Townsend J, Grigoriev IV, Hibbett DS. 2013. Phylogenetic and phylogenomic overview of the *Polyporales*. Mycologia 105: 1350–1373. https://doi.org/10.3852/13-003

Choi JJ, Kim SH. 2017. A genome Tree of life for the fungi kingdom. Proceedings of the National Academy of Sciences of the United States of America 114: 9391–9396. https://doi.org/10.1073/pnas.1711939114

Dai YC. 2010. *Hymenochaetaceae* (*Basidiomycota*) in China. Fungal Diversity 45: 131–343. https://doi.org/10.1007/s13225-010-0066-9

Dai YC. 2012. Polypore diversity in China with an annotated checklist of Chinese polypores. Mycoscience 53: 49–80. https://doi.org/10.1007/s10267-011-0134-3

Dai YC, Yang ZL, Cui BK, Yu CJ, Zhou LW. 2009. Species diversity and utilization of medicinal mushrooms and fungi in China (Review). International Journal of Medicinal Mushrooms 11: 287–302. https://doi.org10.1615/IntJMedMushr.v11.i3.80

Dai YC, Cui BK, Si J, He SH, Hyde KD, Yuan HS, Lui XY, Zhou LW. 2015. Dynamics of the worldwide number of fungi with emphasis on fungal diversity in China. Mycological Progress 14(62). [9 p.] https://doi.org/10.1007/s11557-015-1084-5

Felsenstein J. 1985. Confidence intervals on phylogenetics: an approach using bootstrap. Evolution 39: 783–791. https://doi.org/10.1111/j.1558-5646.1985.tb00420.x

Floudas D, Hibbett DS. 2015. Revisiting the taxonomy of *Phanerochaete* (*Polyporales*, *Basidiomycota*) using a four gene dataset and extensive ITS sampling. Fungal Biology 119: 679–719. https://doi.org/10.1016/j.funbio.2015.04.003

Gilbertson RL, Ryvarden L. 1987. North American polypores 2. *Megasporoporia–Wrightoporia*. Fungiflora, Oslo.

Grigoriev IV, Nikitin R, Haridas S, Kuo A, Ohm R, Otillar R, Riley R, Salamov A, Zhao X, Korzeniewski F, Smirnova T. 2013 ["2014"]. Mycocosm portal: gearing up for 1000 fungal genomes. Nucleic Acids Research 42(D1): D699–D704. https://doi.org/10.1093/nar/gkt1183

Hall TA. 1999. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symposium Series 41: 95–98.

He SH, Li HJ. 2011. *Hymenochaete* in China. 2. A new species and three new records from Yunnan Province. Mycotaxon 118: 411–422. https://doi.org/10.5248/118.411

Justo A, Miettinen O, Floudas D, Ortiz-Santana B, Sjökvist E, Lindner D, Nakasone K, Niemelä T, Larsson KH, Ryvarden L, Hibbett DS. 2017. A revised family-level classification of the *Polyporales* (*Basidiomycota*). Fungal Biology 121: 798–824. https://doi.org/10.1016/j.funbio.2017.05.010

Katoh K, Toh H. 2008. Recent developments in the MAFFT multiple sequence alignment program. Briefings in Bioinformatics 9: 286–298. https://doi.org/10.3767/003158514X681828

Kirk PM, Cannon PF, David JC, Minter DW, Stalpers JA. 2008. Ainsworth and Bisby's dictionary of the fungi. 10th ed. Wallingford, Oxon, UK: CAB International Press. https://doi.org/10.1079/9780851998268.0000

Larsson KH. 2007. Re-thinking the classification of corticioid fungi. Mycological Research 111: 1040–1063. https://doi.org/10.1016/j.mycres.2007.08.001

Levin L, Maira C, Martin H, Rene U. 2016. Degradation of 4-nitrophenol by the white-rot polypore *Trametes versicolor*. International Biodeterioration & Biodegradation 107: 174–179. https://doi.org/10.1016/j.ibiod.2015.11.023

Li HJ, Cui BK. 2010. A new *Trametes* species from Southwest China. Mycotaxon 113: 263–267. https://doi.org/10.5248/113.263

Miettinen O, Rajchenberg M. 2012. *Obba* and *Sebipora*, new polypore genera related to *Cinereomyces* and *Gelatoporia* (*Polyporales*, *Basidiomycota*). Mycological Progress 11: 131–147. https://doi.org/10.1007/s11557-010-0736-8

Miettinen O, Ryvarden L. 2016. Polypore genera *Antella*, *Austeria*, *Butyrea*, *Citripora*, *Metuloidea* and *Trulla* (*Steccherinaceae, Polyporales*). Annales Botanici Fennici 53: 157–172. https://doi.org/10.5735/085.053.0403

Miettinen O, Larsson KH, Sjökvist E, Larsson KL. 2012. Comprehensive taxon sampling reveals unaccounted diversity and morphological plasticity in a group of dimitic polypores (*Polyporales*, *Basidiomycota*). Cladistics 28: 251–270. https://doi.org/10.1111/j.1096-0031.2011.00380.x

Miller MA, Holder MT, Vos R, Midford PE, Liebowitz T, Chan L, Hoover P, Warnow T. 2009. The CIPRES Portals. CIPRES. URL: http://www.phylo.org/sub_sections/portal. 2009-08-04. (Archived by WebCite(r) at http://www.webcitation.org/5imQlJeQa).

Núñez M, Ryvarden L. 2001. East Asian polypores 2. *Polyporaceae* s. lato. Synopsis Fungorum 14: 165–522.

Nylander JAA. 2004. MrModeltest v2. Program distributed by the author. Evolutionary Biology Centre, Uppsala University.

Petersen JH. 1996. Farvekort. The Danish Mycological Society's colour-chart. Foreningen til Svampekundskabens Fremme, Greve.

Posada D, Crandall KA. 1998. Modeltest: testing the model of DNA substitution. Bioinformatics 14: 817–818. https://doi.org/10.1093/bioinformatics/14.9.817

Ronquist F, Huelsenbeck JP. 2003. MrBayes 3: Bayesian phylogenetic inference under mixed models. Bioinformatics 19: 1572–1574. https://doi.org/10.1093/bioinformatics/btg180

Ryvarden L, Melo I. 2014. Poroid fungi of Europe. Synopsis Fungorum 31. 455 p.

Sjökvist E, Larsson E, Eberhardt U, Ryvarden L, Larsson KH. 2012. Stipitate stereoid basidiocarps have evolved multiple times. Mycologia 104: 1046–1055. https://doi.org/10.3852/11-174

Swofford DL. 2002. PAUP*: phylogenetic analysis using parsimony (*and other methods). Version 4.0b10. Sinauer Associates, Massachusetts.

Tomšovský M, Menkis A, Vasaitis R. 2010. Phylogenetic relationships in European *Ceriporiopsis* species inferred from nuclear and mitochondrial ribosomal DNA sequences. Fungal Biology 114: 350–358. https://doi.org/10.1016/j.funbio.2010.02.004

Vu D, Groenewald M, De VM, Gehrmann T, Stielow B, Eberhardt U, Al-Hatmi A, Groenewald JZ, Cardinali G, Houbraken J, Boekhout T, Crous PW, Robert V, Verkley GJM. 2019. Large-scale generation and analysis of filamentous fungal DNA barcodes boosts coverage for kingdom fungi and reveals thresholds for fungal species and higher taxon delimitation. Studies in Mycology 92: 135–154. https://doi.org/10.1016/j.simyco.2018.05.001

Westphalen MC, Rajchenberg M, Tomšovský M, Gugliotta AM. 2018. A re-evaluation of Neotropical *Junghuhnia* s. lat. (*Polyporales, Basidiomycota*) based on morphological and multigene analyses. Persoonia 41: 130–141. https://doi.org/10.3767/persoonia.2018.41.07

White TJ, Bruns T, Lee S, Taylor J. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. 315–322, in: MA Innis & al. (eds). PCR protocols: a guide to methods and applications. Academic Press, San Diego. https://doi.org/10.1016/B978-0-12-372180-8.50042-1

Wu ZQ, Xu TM, Shen S, Liu XF, Luo KY, Zhao CL. 2018. *Elaphroporia ailaoshanensis* gen. et sp nov in *Polyporales* (*Basidiomycota*). MycoKeys 29: 81–95. https://doi.org/10.3897/mycokeys.29.22086

Yang J, He SH. 2014. *Hymenochaete* in China. 8. *H. biformisetosa* sp. nov. with a key to species with denticulate setae. Mycotaxon 128: 137–144. https://doi.org/10.5248/128.137

Yu HY, Zhao CL, Dai YC. 2013. *Inonotus niveomarginatus* and *I. tenuissimus* spp. nov. (*Hymenochaetales*), resupinate species from tropical China. Mycotaxon 124: 61–68. https://doi.org/10.5248/124.61

Zhao CL, Ma X. 2019. *Perenniporia mopanshanensis* sp. nov. from China. Mycotaxon 134: 125–137. https://doi.org/10.5248/134.125

Zhao CL, Wu ZQ. 2017. *Ceriporiopsis kunmingensis* sp. nov. (*Polyporales, Basidiomycota*) evidenced by morphological characters and phylogenetic analysis. Mycological Progress 16: 93–100. https://doi.org/10.1007/s11557-016-1259-8

Zhou LW, Nakasone KK, Burdsall Jr. HH, Ginns J, Vlasák J, Miettinen O, Spirin V, Niemelä T, Yuan HS, He SH, Cui BK, Xing JH, Dai YC. 2016. Polypore diversity in North America with an annotated checklist. Mycological Progress15: 771–790. https://doi.org/10.1007/s11557-016-1207-7

Zmitrovich IV. 2018. Conspectus systematis Polyporacearum v. 1.0. Folia Cryptogamica Petropolitana 6: 3–145.